

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
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Application Serial Number: 10/537,839 A
Source: IFWP
Date Processed by STIC: 08/08/2006

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IFWP

RAW SEQUENCE LISTING

DATE: 08/08/2006

PATENT APPLICATION: US/10/537,839A

TIME: 09:04:22

Input Set : A:\PTO.RJ.TXT

Output Set: N:\CRF4\08082006\J537839A.raw

WITH

3 <110> APPLICANT: Hart, Derek Nigel John
 4 Kato, Masato
 6 <120> TITLE OF INVENTION: DEC-205 (LY 75)/DCL-1 INTERGENIC SPLICE VARIANTS ASSOCIATED
 7 HODGKIN'S DISEASE, AND USES THEREOF
 9 <130> FILE REFERENCE: DAVI257.002APC
 11 <140> CURRENT APPLICATION NUMBER: US 10/537,839A
 12 <141> CURRENT FILING DATE: 2005-06-06
 14 <150> PRIOR APPLICATION NUMBER: PCT/AU03/01634
 15 <151> PRIOR FILING DATE: 2003-12-05
 17 <150> PRIOR APPLICATION NUMBER: AU2002953223
 18 <151> PRIOR FILING DATE: 2002-12-06
 20 <160> NUMBER OF SEQ ID NOS: 32
 22 <170> SOFTWARE: PatentIn version 3.1
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 5622
 26 <212> TYPE: DNA
 27 <213> ORGANISM: mammalian
 29 <220> FEATURE:
 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (1)..(5619)
 34 <400> SEQUENCE: 1

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39 ctg ctc ttc tgg ttc ttc gat ctc gcg gag ccc tct ggc cgc gca gct	96
40 Leu Leu Phe Trp Phe Phe Asp Leu Ala Glu Pro Ser Gly Arg Ala Ala	
41 20 25 30	
43 aat gac ccc ttc acc atc gtc cat gga aat acg ggc aag tgc atc aag	144
44 Asn Asp Pro Phe Thr Ile Val His Gly Asn Thr Gly Lys Cys Ile Lys	
45 35 40 45	
47 cca gtg tat ggc tgg ata gta gca gac gac tgt gat gaa act gag gac	192
48 Pro Val Tyr Gly Trp Ile Val Ala Asp Asp Cys Asp Glu Thr Glu Asp	
49 50 55 60	
51 aag tta tgg aag tgg gtg tcc cag cat cgg ctc ttt cat ttg cac tcc	240
52 Lys Leu Trp Lys Trp Val Ser Gln His Arg Leu Phe His Leu His Ser	
53 65 70 75 80	
55 caa aag tgc ctt ggc ctc gat att acc aaa tcg gta aat gag ctg aga	288
56 Gln Lys Cys Leu Gly Leu Asp Ile Thr Lys Ser Val Asn Glu Leu Arg	
57 85 90 95	
59 atg ttc agc tgt gac tcc agt gcc atg ctg tgg tgg aaa tgt gag cac	336
60 Met Phe Ser Cys Asp Ser Ser Ala Met Leu Trp Trp Lys Cys Glu His	
61 100 105 110	
65 cac tct ctg tac gga gct gcc cgg tac cgg ctg gct ctg aag gat gga	384

(Pg-6)

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71		130					135					140					
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74	Ser	Glu	Glu	Ser	Leu	Cys	Asp	Gln	Pro	Tyr	His	Glu	Ile	Tyr	Thr	Arg	
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77	gat	ggg	aac	tct	tat	ggg	aga	cct	tgt	gaa	ttt	cca	ttc	tta	att	gat	528
78	Asp	Gly	Asn	Ser	Tyr	Gly	Arg	Pro	Cys	Glu	Phe	Pro	Phe	Leu	Ile	Asp	
79				165					170						175		
81	ggg	acc	tgg	cat	cat	gat	tgc	att	ctt	gat	gaa	gat	cat	agt	ggg	cca	576
82	Gly	Thr	Trp	His	His	Asp	Cys	Ile	Leu	Asp	Glu	Asp	His	Ser	Gly	Pro	
83			180					185					190				
85	tgg	tgt	gcc	acc	acc	tta	aat	tat	gaa	tat	gac	cga	aag	tgg	ggc	atc	624
86	Trp	Cys	Ala	Thr	Thr	Leu	Asn	Tyr	Glu	Tyr	Asp	Arg	Lys	Trp	Gly	Ile	
87			195					200					205				
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103			260					265					270				
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106	Ala	Lys	Ile	Phe	Trp	Ile	Gly	Leu	Asn	Gln	Leu	Tyr	Ser	Ala	Arg	Gly	
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115	305				310					315					320		
117	gat	gct	gag	tct	ggg	ctg	tgg	cag	agc	ttt	tcc	tgt	gaa	gct	caa	ctg	1008
118	Asp	Ala	Glu	Ser	Gly	Leu	Trp	Gln	Ser	Phe	Ser	Cys	Glu	Ala	Gln	Leu	
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122	Pro	Tyr	Val	Cys	Arg	Lys	Pro	Leu	Asn	Asn	Thr	Val	Glu	Leu	Thr	Asp	
123			340					345					350				
125	gtc	tgg	aca	tac	tca	gat	acc	cgc	tgt	gat	gca	ggc	tgg	ctg	cca	aat	1104
126	Val	Trp	Thr	Tyr	Ser	Asp	Thr	Arg	Cys	Asp	Ala	Gly	Trp	Leu	Pro	Asn	
127			355					360					365				
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137	tct cta gca gat gtg gag gtg gtt gtc aca aaa ctc cat aat gag gat	1248		
138	Ser Leu Ala Asp Val Glu Val Val Val Thr Lys Leu His Asn Glu Asp			
139	405 410 415			
141	atc aaa gaa gaa gtg tgg ata ggc ctt aag aac ata aac ata cca act	1296		
142	Ile Lys Glu Glu Val Trp Ile Gly Leu Lys Asn Ile Asn Ile Pro Thr			
143	420 425 430			
145	tta ttt cag tgg tca gat ggt act gaa gtt act cta aca tat tgg gat	1344		
146	Leu Phe Gln Trp Ser Asp Gly Thr Glu Val Thr Leu Thr Tyr Trp Asp			
147	435 440 445			
149	gag aat gag cca aat gtt ccc tac aat aag acg ccc aac tgt gtt tcc	1392		
150	Glu Asn Glu Pro Asn Val Pro Tyr Asn Lys Thr Pro Asn Cys Val Ser			
151	450 455 460			
153	tac tta gga gag cta ggt cag tgg aaa gtc caa tca tgt gag gag aaa	1440		
154	Tyr Leu Gly Glu Leu Gly Gln Trp Lys Val Gln Ser Cys Glu Glu Lys			
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175	545 550 555 560			
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180	Arg Asp Val Asp Ser Cys Gly Glu Tyr Asn Trp Ala Thr Val Gly Gly			
181	565 570 575			
183	aga agg cgg gct gta acc ttt tcc aac tgg aat ttt ctt gag cca gct	1776		
184	Arg Arg Arg Ala Val Thr Phe Ser Asn Trp Asn Phe Leu Glu Pro Ala			
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188	Ser Pro Gly Gly Cys Val Ala Met Ser Thr Gly Lys Ser Val Gly Lys			
189	595 600 605			
191	tgg gag gtg aag gac tgc aga agc ttc aaa gca ctt tca att tgc aag	1872		
192	Trp Glu Val Lys Asp Cys Arg Ser Phe Lys Ala Leu Ser Ile Cys Lys			
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197	625 630 635 640			

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208	Glu	Ala	Glu	Arg	Phe	Cys	Gln	Ala	Leu	Gly	Ala	His	Leu	Ser	Ser	Phe	
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212	Ser	His	Val	Asp	Glu	Ile	Lys	Glu	Phe	Leu	His	Phe	Leu	Thr	Asp	Gln	
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217	705					710					715					720	
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241					805					810					815		
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251	act	ata	aca	tct	ttt	gtg	gga	cta	aaa	gcc	atc	aaa	aac	aaa	ata	gca	2592
252	Thr	Ile	Thr	Ser	Phe	Val	Gly	Leu	Lys	Ala	Ile	Lys	Asn	Lys	Ile	Ala	
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256	Asn	Ile	Ser	Gly	Asp	Gly	Gln	Lys	Trp	Trp	Ile	Arg	Ile	Ser	Glu	Trp	
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260	Pro	Ile	Asp	Asp	His	Phe	Thr	Tyr	Ser	Arg	Tyr	Pro	Trp	His	Arg	Phe	
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268 Leu Ile Asp Leu Gly Lys Pro Thr Asp Cys Ser Thr Lys Leu Pro Phe
269          915          920          925
271 atc tgt gaa aaa tat aat gtt tct tcg tta gag aaa tac agc cca gat      2832
272 Ile Cys Glu Lys Tyr Asn Val Ser Ser Leu Glu Lys Tyr Ser Pro Asp
273          930          935          940
275 tct gca gct aaa gtg caa tgt tct gag caa tgg att cct ttt cag aat      2880
276 Ser Ala Ala Lys Val Gln Cys Ser Glu Gln Trp Ile Pro Phe Gln Asn
277 945          950          955          960
279 aag tgt ttt cta aag atc aaa ccc gtg tct ctc aca ttt tct caa gca      2928
280 Lys Cys Phe Leu Lys Ile Lys Pro Val Ser Leu Thr Phe Ser Gln Ala
281          965          970          975
283 agc gat acc tgt cac tcc tat ggt ggc acc ctt cct tca gtg ttg agc      2976
284 Ser Asp Thr Cys His Ser Tyr Gly Gly Thr Leu Pro Ser Val Leu Ser
285          980          985          990
287 cag att gaa caa gac ttt att aca tcc ttg ctt ccg gat atg gaa gct      3024
288 Gln Ile Glu Gln Asp Phe Ile Thr Ser Leu Leu Pro Asp Met Glu Ala
289          995          1000          1005
293 act tta tgg att ggt ttg cgc tgg act gcc tat gaa aag ata aac      3069
294 Thr Leu Trp Ile Gly Leu Arg Trp Thr Ala Tyr Glu Lys Ile Asn
295          1010          1015          1020
297 aaa tgg aca gat aac aga gag ctg acg tac agt aac ttt cac cca      3114
298 Lys Trp Thr Asp Asn Arg Glu Leu Thr Tyr Ser Asn Phe His Pro
299          1025          1030          1035
301 tta ttg gtt agt ggg agg ctg aga ata cca gaa aat ttt ttt gag      3159
302 Leu Leu Val Ser Gly Arg Leu Arg Ile Pro Glu Asn Phe Phe Glu
303          1040          1045          1050
305 gaa gag tct cgc tac cac tgt gcc cta ata ctc aac ctc caa aaa      3204
306 Glu Glu Ser Arg Tyr His Cys Ala Leu Ile Leu Asn Leu Gln Lys
307          1055          1060          1065
309 tca ccg ttt act ggg acg tgg aat ttt aca tcc tgc agt gaa cgc      3249
310 Ser Pro Phe Thr Gly Thr Trp Asn Phe Thr Ser Cys Ser Glu Arg
311          1070          1075          1080
313 cac ttt gtg tct ctc tgt cag aaa tat tca gaa gtt aaa agc aga      3294
314 His Phe Val Ser Leu Cys Gln Lys Tyr Ser Glu Val Lys Ser Arg
315          1085          1090          1095
317 cag acg ttg cag aat gct tca gaa act gta aag tat cta aat aat      3339
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319          1100          1105          1110
321 ctg tac aaa ata atc cca aag act ctg act tgg cac agt gct aaa      3384
322 Leu Tyr Lys Ile Ile Pro Lys Thr Leu Thr Trp His Ser Ala Lys
323          1115          1120          1125
325 agg gag tgt ctg aaa agt aac atg cag ctg gtg agc atc acg gac      3429
326 Arg Glu Cys Leu Lys Ser Asn Met Gln Leu Val Ser Ile Thr Asp
327          1130          1135          1140
329 cct tac cag cag gca ttc ctc agt gtg cag gcg ctc ctt cac aac      3474
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:10; Xaa Pos. 5,13,142

Seq#:11; Xaa Pos. 5,13,142

Seq#:13; N Pos. 43

VERIFICATION SUMMARY

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L:1830 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:48
M:341 Repeated in SeqNo=10
L:1920 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
M:341 Repeated in SeqNo=11
L:2029 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0